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Letter to the Editor

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In the year 2000, Oelrichs et al. reported the presence of HIV-1 subtype C in Nepal (3). These findings were based on the *env* gene sequences from 36 HIV-1 patients. They reported that Nepali HIV sequences showed a close clustering pattern with the Indian reference sequences, indicating the origin of HIV-1 subtype C in India (3). Since that report, no subtyping data have been reported from Nepal. In 11 years' time, there is a possibility that new viral strains may have been introduced into the Nepalese population. From samples collected from the people living with HIV/AIDS (PLHIV) community representing different most at-risk population (MARP) groups in 2010, we performed a subtype analysis of HIV samples from Nepal. HIV *gag* and *pol* regions were successfully amplified in a nested PCR from 10 HIV-positive samples from Nepal. The amplified products were sequenced subsequently and deposited into the National Center for Biotechnology Information. The subtypes were assigned to the samples based on the closest homology found with the subtype references in the HIV Los Alamos database.

All except one sample were found to be subtype C, showing close homology with the HIV subtype C sequences from India (data not shown); this was in congruence with the results of Oelrichs et al. (3). However, one sample, collected from a Nepalese HIV-positive migrant worker, was found to be HIV-1 CRF01_AE. Using the HIV BLAST search (<http://www.hiv.lanl.gov/>), the CRF01_AE sample showed more than 90% homology to HIV *gag* sequences from Thailand. This is the first instance of an HIV circulating recombinant form (CRF) found in Nepal. The studies reported so far have shown the origin of subtype C in Nepal to be from India. A heavy traffic of migrant workers across the India-Nepal border makes that observation plausible. Our analysis shows a likelihood of HIV transmission from Thailand.

Population mobility has been reported as a major factor in HIV spread in Nepal, with male laborers and female sex workers being the high-risk groups carrying HIV into the population (2). It is possible that new viral strains are being introduced through the same routes into Nepal from countries other than India. Moreover, considering the movement of Nepalese migrant workers to different countries within Asia (1), and taking into account the history of the CRF01_AE-positive Nepalese subject we studied, it is possible that the

CRF reported here was also transmitted into Nepal through cross-border migration. A wider sample collection and further analysis should be performed to chart the shifting patterns of the HIV epidemic in the Nepalese population.

Nucleotide sequence accession numbers. The amplified products from the subtype analysis were deposited into the National Center for Biotechnology Information under accession numbers JN023031 to JN023040.

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